From: Swope, Sheridan
Sent: Monday, March 03, 2003 8:11 PM
To: STIC-ILL
Subject: 09917376

GREETINGS!!!

I need copies of:
Tomme P et al 1995, in Enzymatic Degradation of Insoluble Polysaccharides (Saddler and Penner, eds) at 142-163, American Chemical Society, Washington.

Gilkes NR, Warren RA, Miller RC Jr, Kilburn DG.
Precise excision of the cellulose binding domains from two Cellulomonas fimi cellulases by a homologous protease and the effect on
        catalysis.
        J Biol Chem. 1988 Jul 25;263(21):10401-7.

THANKS!!!

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General Description References Links Sequence

General information

Entry name	**O74170**
Accession number	**O74170**
Created	TrEMBLrel. 08, 1-NOV-1998
Sequence update	TrEMBLrel. 08, 1-NOV-1998
Annotation update	TrEMBLrel. 22, 1-OCT-2002

Description and origin of the Protein

Description	Avicelase III.
Gene name(s)	AVIIII.
Organism source	Aspergillus aculeatus.
Taxonomy	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI TaxID	5053

References

[1] Arai,M., Takada,G., Kawaguchi,T., Sumitani,J.,
Avicelase III from Aspergillus aculeatus. Submitted JUN-1998 to the EMBL GenBank DDBJ databases

Position SEQUENCE FROM N.A.

Database cross-references

EMBL	AB015511; BAA29031.1; -.
HSSP	P00725; 2CBH.
InterPro	IPR000254; CBD_fungal.
	IPR002860; GH_BNR.
Pfam	PF02012; BNR; 7.
	PF00734; CBM_1; 1.
ProDom	PD001821; CBD_fungal; 1.
SMART	SM00236; fCBD; 1.
PROSITE	PS00562; CBD_FUNGAL; 1.

Sequence information

Length: **856 aa**, molecular weight: **89820 Da**, CRC64 checksum: **BE085983AF60ED76**

```
        MARSSLALLC AALLGKLADA AASQAYTWKN VVTGGGGGFT PGIVFNPSAK GVAYARTDIG      60
        GAYRLNSDDT WTPLMDWVGN DTWHDWGIDA LATDPVDTDR VYVAVGMYTN EWDPNVGSIL     120
        RSTDQGDTWT ETKLPFKVGG NMPGRGMGER LAVDPNKNSI LYFGARSGHG LWKSTDYGAT     180
        WSNVTSFTWT GTYFQDSSST YTSDPVGIAW VTFDSTSGSS GSATPRIFVG VADAGKSVFK     240
        SEDAGATWAW VSGEPQYGFL PHKGVLSPEE KTLYISYANG AGPYDGTNGT VHKYNITSGV     300
        WTDISPTSLA STYYGYGGLS VDLQVPGTLM VAALNCWWPD ELIFRSTDSG ATWSPIWEWN     360
        GYPSINYYYS YDISNAPWIQ DTTSTDQFPV RVGWMVEALA IDPFDSNHWL YGTGLTVYGG     420
        HDLTNWDSKH NVTVKSLAVG IEEMAVLGLI TPPGGPALLS AVGDDGGFYH SDLDAAPNQA     480
        YHTPTYGTTN GIDYAGNKPS NIVRSGASDD YPTLALSSNF GSTWYADYAA STSTGTGAVA     540
        LSADGDTVLL MSSTSGALVS KSQGTLTAVS SLPSGAVIAS DKSDNTVFYG GSAGAIYVSK     600
        NTATSFTKTV SLGSSTTVNA IRAHPSIAGD VWASTDKGLW HSTDYGSTFT QIGSGVTAGW     660
```

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SFGFGKASST GSYVVIYGFF TIDGAAGLFK SEDAGTNWQV ISDASHGFGS GSANVVNGDL      720
QTYGRVFRGH ERPGHLLRQS QREPAGRHGD GDGDTTTSKT STTVSTTLKT TTSSASTTSS      780
STTVKTTTSS SSTTSKASST TTTKTTTTST TTSSGTTATA SAYAQCGGNG WTGATVCFTG      840
YTCTYSNAFY SQCVPS                                                      856
```

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CBD

General Description References Links Sequence

```
ID   CBD_FUNGAL; PATTERN.
AC   PS00562;
DT   DEC-1991 (CREATED); NOV-1997 (DATA UPDATE); JUL-1998 (INFO UPDATE).
DE   Cellulose-binding domain, fungal type.
PA   C-G-G-x(4,7)-G-x(3)-C-x(5)-C-x(3,5)-[NHG]-x-[FYWM]-x(2)-Q-C.
NR   /RELEASE=40.7,103373;
NR   /TOTAL=22(19); /POSITIVE=22(19); /UNKNOWN=0(0); /FALSE_POS=0(0);
NR   /FALSE_NEG=1; /PARTIAL=0;
CC   /TAXO-RANGE=??E??; /MAX-REPEAT=4;
CC   /SITE=1,disulfide; /SITE=7,disulfide; /SITE=9,disulfide;
CC   /SITE=16,disulfide;
DR   Q00023, CEL1_AGABI, T; Q12714, GUN1_TRILO, T; P07981, GUN1_TRIRE, T;
DR   P07982, GUN2_TRIRE, T; Q12624, GUN3_HUMIN, T; P43317, GUN5_TRIRE, T;
DR   P46236, GUNB_FUSOX, T; P46239, GUNF_FUSOX, T; P45699, GUNK_FUSOX, T;
DR   P15828, GUX1_HUMGR, T; Q06886, GUX1_PENJA, T; P13860, GUX1_PHACH, T;
DR   P00725, GUX1_TRIRE, T; P19355, GUX1_TRIVI, T; Q92400, GUX2_AGABI, T;
DR   P07987, GUX2_TRIRE, T; P49075, GUX3_AGABI, T; P46238, GUXC_FUSOX, T;
DR   P50272, PSBP_PORPU, T;
DR   O59843, GUX1_ASPAC, N;
3D   1AZ6; 1AZH; 1AZK; 1CBH; 2CBH;
DO   PDOC00486;
//
```

S GG -x(12) -G -x(42) -G -x(8)-N -x(5) -G -x

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Search in PROSITE for: glycosyl hydrolase family 74

(Release 17.38, of 23-Feb-2003)

No data or consensus sequence

Enter search keywords:

```
glycosyl hydrolase family 74
```

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| new search | | clear |

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The request is performed as:
glycosyl hydrolase AND hydrolase family AND family 74

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InterPro

InterPro Entry IPR003305

Carbohydrate-binding, CenC-like

Database	InterPro
Accession	IPR003305; CBM_CenC (matches 97 proteins)
Name	Carbohydrate-binding, CenC-like
Type	Domain ⓘ
Dates	14-NOV-2000 (created) 12-FEB-2001 (last modified)
Signatures	PF02018; CBM_4_9 (97 proteins)
Abstract ⓘ	The 1,4-beta-glucanase CenC from Cellulomonas fimi contains two cellulose-binding domains, CBD(N1) and CBD(N2), arranged in tandem at its N-terminus. These homologous CBDs are distinct in their selectivity for binding amorphous and not crystalline cellulose [1]. Multidimensional heteronuclear nuclear magnetic resonance (NMR) spectroscopy was used to determine the tertiary structure of the 152 amino acid N-terminal cellulose-binding domain from Cellulomonas fimi 1,4-beta-glucanase CenC (CBDN1)[2]. The tertiary structure of CBDN1 is strikingly similar to that of the bacterial 1,3-1,4-beta-glucanases, as well as other sugar-binding proteins with jelly-roll folds.
Examples	• Q53317 XYND_RUMFL • P40944 XYNA_CALSR • Q05156 GUN1_STRRE • P14090 GUNC_CELFI • Q05638 CHIX_STROI View examples
References	1. Brun E., Johnson P.E., Creagh A.L., Tomme P., Webster P., Haynes C.A., McIntosh L.P. *Structure and binding specificity of the second N-terminal cellulose-binding domain from Cellulomonas fimi endoglucanase C.* Biochemistry 39(10): 2445-2458(2000). [MEDLINE:20170870] 2. Johnson P.E., Joshi M.D., Tomme P., Kilburn D.G., McIntosh L.P. *Structure of the N-terminal cellulose-binding domain of Cellulomonas fimi CenC determined by nuclear magnetic resonance spectroscopy.* Biochemistry 35(45): 14381-14394(1996). [MEDLINE:97074498]
Matches ⓘ	Table all Graphical all Condensed graphical view

```
O42181/201-285       YVACLKESSSGGGAERSELV.IFSSSTPGNFTR.EQCNSVCFTASHRYGGLGGRHECLCSTNSI
O08852/180-261       YVACLPDNSSGAVAA....V.PFYFAHEGPLET.EACSAFCFSAGEGLAALSEQNQCLCGAGQA.
PKD1_HUMAN/180-261    YVACLPDNSSGTVAA....V.SFSAAHEGLLQP.EACSAFCFSTGQGLAALSEQGWCLCG.
Q12215/42-122        YEGCY..SAADIQS....A.GLSLKNSYIYQSVSYCQNQCP..ESAVVALFNGSDCYCGNSVSFLTS
YN23_YEAST/28-108    YKACY..SASDIRK....I.GLTYKGVYEYQSVSYCQNECP..GQAVVALFNGTGCYCGGSVI
YLU2_PICAN/18-91     YLGCY..SSDAIS.......GLTKKDSYTWQSSSHCTEQCS..GHAVAALINGQDCYCGDDVP.....
SLG1_YEAST/24-100    YVNCF.....SSLPS......DFSKADSYNWQSSSHCNSECSAKGASYFALYNHSECYCGDTNP...
YHC8_YEAST/28-99     QSVCS..SQN........T.ATTDGVRNQFQSNGWCSNNCAG...HQFAIVQGFMCWCSDSEP....S
O60276/38-117        YIGCFS..DDGHERT....I.KGAVFYDLRKMTVSHCQDACAERSYVYAGLEAGAECYCGNRLP.
O14402/819-904       FLGCYS..DNVNGRT...LANQVQVAGGASAMSIEACETASESAGYTIAGVEYSGECWCDTKF
O14402/930-1014      FRGCYT..DSVNARA...LI.AESVPNGPSSMTIEACQSVCKGLGYTLAGLEYADECYCGNSLA
```

```
O42181/201-285       CTNP...QVMEVIG
O08852/180-261       CSSISLSLNSACGG
PKD1_HUMAN/180-261      CSGPPAPPAPTCRG
Q12215/42-122        CSGWPYQM...CGG
YN23_YEAST/28-108     CAGWPYQN...CGG
YLU2_PICAN/18-91     CTGYPMEK...CGG
SLG1_YEAST/24-100     CFGYSSEM...CGG
YHC8_YEAST/28-99      CPGYGYED...CGN
O60276/38-117        CKGEKGSV...CGA
O14402/819-904       CSGAPQET...CGG
O14402/930-1014      CAGNAAET...CGG
```

The coloured markup was created by Jalview (Michele Clamp)

Alignments are colored using the ClustalX scheme in Jalview (orange:glycine (G); yellow: Proline (P); blue: small and hydrophobic amino-acids (A, V, L, I, M, F, W); green: hydroxyl and amine amino-acids (S, T, N, Q); red: charged amino-acids (D, E, R, K); cyan: histidine (H) and tyrosine(Y)).